REMARKS

The Examiner notes that a Sequence Listing is required under U.S. rules of practice. A Sequence Listing is enclosed herewith as discussed below.

The Amendments

Claims 1 and 15 are amended herein to specifically recite exon17/intron as the site of the mutation correlated with coat color for the purposes of this invention. This amendment is supported, *inter alia*, on page 5, lines 4-27.

The Rejections

The Examiner has rejected claims 1, 4, 5, 8, and 10-16 as insufficiently supported by the specification. The Examiner acknowledges that the specification discloses an alteration in splice site of intron 17 which is associated with specific coat color. Claims 1 and 15 are amended herein to specifically recite exon17/intron as the site of the mutation correlated with coat color for the purposes of this invention.

The Examiner has objected to claim language in claims 1, 3, 5, 14, and 15. For claims 1, 14 and 15, the Examiner argues that there is no correspondence between the preamble and the body of the claims. This has been addressed by adding a clause at the end of the claim relating the successful result of the method to the preamble. The remaining issues of claim language were addressed in a preliminary amendment which is not acknowledged in this Office Action.

The only prior art rejection is a rejection of claim 15 over Moller (1996) which discloses primers for amplifying a portion of the kit gene. The Examiner argues that claim 15 reads on the primers disclosed by Moller. The amendment of cliam 15 above excludes the primer amplification of Moller, and therefore, this prior art rejection should be withdrawn.

Submission of Sequence Listing

Applicants enclose herewith a paper copy of a properly formatted Sequence Listing and a computer readable copy (diskette) of the Sequence Listing in accordance with the requirements of 37 C.F.R. §§ 1.821-1.825. Applicants hereby state that the content of the paper copy and computer readable copy of the Sequence Listing, submitted in accordance with 37

C.F.R. § 1.821(c) and (e), respectively, are the same, and that this submission does not include any new matter.

CONCLUSION

Applicant respectfully submits that this application is in condition for allowance, and such disposition is earnestly solicited. If the Examiner believes that the prosecution might be advanced by discussing the application with Applicant's representatives, in person or over the telephone, we would welcome the opportunity to do so.

Respectfully submitted,

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APPENDIX A

CLAIMS WITH MARKINGS

In accordance with 37 C.F.R. § 1.12(b), Applicants submit herewith a marked version of claims 1, 14 and 15, in order to indicate the changes Applicants have made to these claims.

1. (Amended) A method for determining coat colour genotype in a pig which comprises:

(a) obtaining a sample of pig nucleic acid; and

(b) analysing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at [one or more] an exon 17/intron splice [sites] site of *KIT* gene, wherein presence or absence of said mutation is correlated with coat color.

2. A method as claimed in claim 1 wherein the analysis in step (b) is carried out to determine whether a mutation is/is not present at the exon 17/intron 17 boundary.

3. A method is claimed in claim 2 wherein the mutation consists of the substitution of the G of the conserved GT pair for A.

4. A method as claimed in claim 1 wherein the sample of nucleic acid is amplified prior to analysis.

5. A method as claimed in claim 4 wherein the nucleic acid is genomic DNA.

6. A method as claimed in claim 5 wherein amplification is carried out using PCR and at least one pair of suitable primers.

7. A method as claimed in claim 6 wherein the pair of suitable primers is:

5'-GTA TTC ACA GAG ACT TGG CGG C-3'); and

5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3'.

8. A method as claimed in claim 5 wherein after amplification the nucleic acid is treated with a restriction enzyme, followed by analysis of fragment lengths.

9. A method as claimed in claim 8 wherein the nucleic acid is treated with the restriction enzyme *Nla*III.

10. A method as claimed in claim 8 or claim 9 wherein the ratio of restriction fragment lengths is determined.

11. A method as claimed in claim 4 wherein the nucleic acid is mRNA.

12. A method as claimed in claim 11 wherein the nucleic acid is amplified using RT-PCR.

13. A method as claimed in claim 12 wherein the length of RT-PCR product is determined.

14. (Amended) A method for determining coat colour genotype in a pig which comprises the step of analysing a sample of pig KIT protein to determine whether the protein is the splice variant protein, said protein being correlated with coat color.

15. (Amended) A kit for use in determining the coat colour genotype of a pig which comprises one or more reagents suitable for determining whether a mutation is present at [one or more] an exon 17/intron splice [sites] site of the *KIT* gene, wherein presence or absence of said mutation is correlated with coat color..

16. A kit as claimed in claim 15 which comprises one or more reagents for carrying out PCR and one or more pairs of suitable primers.

17. A kit as claimed in claim 16 which comprises the following pair of primers:

5'-GTA TTC ACA GAG ACT TGG CGG C-3'); and

5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3'.